

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 07:42:35 ; Search time 28 Seconds
(without alignments)
1209.582 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDYQVSSPIVDINYITSEPC.....ERASSVYTRTGEISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79.*

2: pir1.*

3: pir2.*

4: pir3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	2 A43113	chemokine (C-C) re
2	1359	73.8	360	2 JC2443	chemokine (C-C) re
3	1219	66.2	374	2 I38450	chemokine (C-C) re
4	1059	57.5	355	2 A45177	chemokine (C-C) re
5	1011.5	54.9	355	2 I49339	macrophage inflam
6	1003.5	54.5	359	2 I49341	MIP-1 alpha recept
7	936.5	50.9	355	2 G02436	chemokine (C-C) re
8	914	49.6	360	2 A57160	chemokine (C-C) re
9	901	48.9	360	2 JC4587	chemokine (C-C) re
10	832	45.2	383	2 S55594	G protein-coupled
11	802.5	43.6	356	2 I49340	MIP-1 alpha recept
12	751.5	40.8	355	2 JC5067	G protein-coupled
13	717	38.9	354	2 I58186	probable G protein
14	675.5	36.7	355	2 JC4304	orphan G protein-c
15	670	36.4	344	2 JC5942	chemokine receptor
16	562	30.4	378	2 B55735	lymphocyte-specifi
17	560	30.5	378	2 A55735	G protein-coupled
18	554	30.1	369	2 JC5068	G protein-coupled
19	548	29.8	378	2 A45680	G protein-coupled
20	542	29.4	333	2 I65989	G protein-coupled
21	520	28.2	360	2 A53611	interleukin-8 rece
22	516.5	28.1	359	2 A48921	interleukin-8 rece
23	514	27.9	355	2 JQ1231	interleukin-8 rece
24	513.5	27.9	358	2 A53752	interleukin-8 rece
25	505.5	27.5	350	2 A39445	interleukin-8 rece
26	505.5	27.5	350	2 A39445	interleukin-8 rece
27	504.5	27.4	367	2 JN0621	interferon-inducib
28	501	27.2	352	2 G00048	G protein-coupled
29	501	27.2	352	2 A45747	neuropeptide Y/pep

30 491.5 26.7 353 2 S28787 neuropeptide Y/pep
31 489.5 26.6 356 2 J42096 interleukin-8 rece
32 473.5 25.7 359 2 JC2134 angiotensin II rec
33 472.5 25.7 359 2 A42656 angiotensin II rec
34 470 25.5 359 2 I51372 angiotensin II rec
35 468.5 25.4 359 2 JH0621 angiotensin II rec
36 468 25.4 374 2 S42628 G protein-coupled
37 467.5 25.4 359 2 S44425 angiotensin II rec
38 467.5 25.4 359 2 JCL1194 angiotensin II rec
39 465.5 25.3 359 2 S15403 angiotensin II rec
40 463.5 25.2 359 2 JQ1516 angiotensin II rec
41 460.5 25.0 359 2 JC1104 angiotensin II rec
42 459.5 25.0 359 2 A48857 angiotensin II rec
43 457 24.8 327 2 S56162 MDCR15 protein - h
44 457 24.8 372 2 S26667 G protein-coupled
45 449 24.4 374 2 S32785 G protein-coupled

ALIGNMENTS

RESULT 1

A43113

chemokine (C-C) receptor. 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine recept

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:G1262810; PIDN:CAAG2796.1; PID:G1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosa

M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; P

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184,'INDSLGAGPAAACHGILLGNPKNSASVSK' <SAM3>

A;Cross-references: GB:X9393; NID:G1524062; PIDN:CAAG7767.1; PID:G1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a deg

nd may have had a selective advantage by conferring resistance to Yersinia plague infec

R;Combadiere, C.; Anuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine re

A;Reference number: A58832; MUID:96295970; PMID:8699119

A;Accession: A58832

A;Molecule type: mRNA

A;Residues: 1-352 <COM1>

A;Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409

A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R;Combadiere, C.

submitted to the EMBL Data Library, May 1996

A;Reference number: H01541

A;Accession: G02653

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-89,'L',91-352 <COM2>

A;Cross-references: EMBL:U57840

R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A;Title: Molecular cloning and functional characterization of a novel human CC chemokin

A;Reference number: A58833; MUID:96291862; PMID:8663314

A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575), and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 2, splice form B - human
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A;Note: Probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
F;32-56/Domain: transmembrane #status predicted <TM1>
F;32-56/Domain: transmembrane #status predicted <TM2>
F;67-87/Domain: transmembrane #status predicted <TM3>
F;103-124/Domain: transmembrane #status predicted <TM4>
F;142-166/Domain: transmembrane #status predicted <TM5>
F;193-218/Domain: transmembrane #status predicted <TM6>
F;236-257/Domain: transmembrane #status predicted <TM7>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carboxylate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 99.7%; Score 1836; DB 2; Length 352;
Best Local Similarity 99.7%; Pred. No. 7.2e-143;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSILVIFGFGVNMVLVILLINCKR 60
DB 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSILVIFGFGVNMVLVILLINCKR 60

QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIPFII 120
DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIPFII 120

QY 121 LLTIDRYLAVVHAFVFKARTVTGGVVTITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFVFKARTVTGGVVTITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180

QY 181 HPYSQYQFKNQFTLKIIVILGVLPLLVNVIYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPYSQYQFKNQFTLKIIVILGVLPLLVNVIYSGILKTLRCRNEKKHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIYLLNTQEFPGNNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIYLLNTQEFPGNNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 352

RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 2, splice form A - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BA06253.1; PID:g531246
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;81-100/Domain: transmembrane #status predicted <TM1>
F;115-136/Domain: transmembrane #status predicted <TM2>
F;154-178/Domain: transmembrane #status predicted <TM3>
F;207-226/Domain: transmembrane #status predicted <TM4>
F;244-268/Domain: transmembrane #status predicted <TM5>
F;287-309/Domain: transmembrane #status predicted <TM6>
F;14/Binding site: carboxylate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 73.8%; Score 1359; DB 2; Length 360;
Best Local Similarity 75.2%; Pred. No. 7.8e-104;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 10 YDINYYTSEPCQKINVKQIAARLLPPLYSILVIFGFGVNMVLVILLINCKRSMTDIYL 69
DB 24 FDYDY--GAPCHKDFVKQICAGQLPPLYSILVIFGFGVNMVLVILLINCKRSMTDIYL 81

QY 70 LNLAIISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIPFIIITIDRYLA 129
DB 82 LNLAIISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIPFIIITIDRYLA 141

QY 130 VVHAFVFKARTVTGGVVTITVWVAVFASLPGLIIFTRSQEGLHYTCSSHPYSQYQF 189
DB 142 VVHAFVFKARTVTGGVVTITVWVAVFASLPGLIIFTRSQEGLHYTCSSHPYSQYQF 197

QY 190 WKNFOTLKIVILGVLPLLVNVIYSGILKTLRCRNEKKHRAVRLIFTIMIVYFLFWA 249
DB 198 WNNFHTIMRNLGLVPLLVNVIYSGILKTLRCRNEKKHRAVRLIFTIMIVYFLFWT 257

QY 250 PYNIVLLNTQEFPGNNCSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 309
DB 258 PYNIVLLNTQEFPGNNCSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 317

QY 310 VPFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
DB 318 VPFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 360

RESULT 3
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 2, splice form A - human
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472555
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted

Query Match	66.2%;	Score 1219;	DB 2;	Length 374;
Best Local Similarity	76.0%;	Pred. No. 2.3e-92;		
Matches 234;	Conservative 27;	Mismatches 35;	Indels 12;	Gaps 3;

Qy	10	YDINYITSEPCOKINVAQIARLLPPYLSLVIFGFVGNMLVILILINCKRLKMSMTDIYL	69
Db	24	FDYDI--GAPCHKEDVQIQAGLQAPPLYSLVIFGFVGNMLVILILINCKRLKCLTDIYL	81
Qy	70	LNLAISDLFFLLITVPFWAHYLAQWDFGNTMCQLLTGLYFTIGFSGIFFIILLTIDRYLA	129
Db	82	LNLAISDLLFLITLPLWAHSAANEWFVGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA	141
Qy	130	VHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSHPPYSQYQF	189
Db	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKQKEDSVVVCGPYFP---RG	197
Qy	190	WKNPQTLKIVILGHAVLPLLVWVICYSGILKTLLECRNEKXHRRAVRLIFITMIVYFLFWA	249
Db	198	WNNPHTIMRNILGHAVLPLLVWVICYSGILKTLLECRNEKXHRRAVRVIFITMIVYFLFWT	257
Qy	250	PYNIVLLINTFOEFPFGLNCCSSNRLDQAMQVETLGNTHCCINPIIYAFVGEKFRNYLL	309
Db	258	PYNIVLLINTFOEFPFGLSNCEISQLDQATQVETLGNTHCCINPIIYAFVGEKFRSLF-	316
Qy	310	VFFQKHIA	317
Db	317	-----HIA	319

RESULT 4
A45177
Chemokine (C-C) receptor 1 - human
N;Alternate-names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NBO>
A;Cross-references: UNIPROT:P32246; GB:L01918; NID:G292416; PIDN:AAA36543.1; PID:G92417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

B. Exp. Med. 177, 1421-1421, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A:Reference number: I55671; MUID:93240122; PMID:7683036
 A:Accession: I55671
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:
 A:Gene: GDB:CMKBK1; CMKR-1
 A:Cross-references: GDB:L38446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr

F/36-60/Domain: transmembrane #status predicted <TM1>
F/71-91/Domain: transmembrane #status predicted <TM2>
F/108-129/Domain: transmembrane #status predicted <TM3>
F/147-171/Domain: transmembrane #status predicted <TM4>
F/205-223/Domain: transmembrane #status predicted <TM5>
F/240-264/Domain: transmembrane #status predicted <TM6>
F/288-305/Domain: transmembrane #status predicted <TM7>
F/5/Binding site: carbohydrate (Asn) (covalent) #status predicted
P/24-273,106-183/Disulfide bonds: #status predicted
P/345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match	57.5%;	Score 1059;	DB 2;	Length 355;	
Best Local Similarity	56.4%;	pred. No. 2.7e-79;			
Matches	198;	Conservative 59;	Mismatches 88;	Indels 6;	Gaps 4;
Qy	2	DYQVSSPIYDINYTSBPCQKINVKQTAARLLPPLYSLVFIFGFGVGNMLVLIILNCKRL	61		
Db	9	DYDTT---BFDYGDATPCQKVERAFAQQLPPLYSLVFIVGLVGNLVLVLVQYKRL	65		
Qy	62	KSMTDIIYLLNLAISDLFLFLTVPRWAHY-LAAQDQFGNTMCQLLTGLYFIFGPFSGIFFI	120		
Db	66	KWMTSIYLLNLAISDLFLFLTPWIDYKLDKDDWFGDMCKILSGFYTTGYSIEIFFII	125		
Qy	121	LLATIDRYLAVVHAFALKARTVTTFGVTSVITWVAVPASLPFGIIFTRSQKGLHYTCSS	180		
Db	126	LLATIDRYLAVHAFALRARTVTTFGVTSIIIIWALAIIASMPGLYFSKTQWEFTHTCSL	185		
Qy	181	HPYYSQVQWKNFOTLKIVILGLVPLPWWVCYSGILKTLRLCRNCKRQHRAVLFIPT	240		
Db	186	HFPHESUREKWLFOALKNLNLFGLVPLPWLVIICYTGIIKIILRRPNKK-SKAVRLIFVI	244		
Qy	241	MIVVFLPWPVNIIVLLANTQERFGLNCCSSNRLDQAMQVTELTGMTHCCINPLIYAVP	300		
Db	245	MIILFFWTPTNLIISVDFLFTHECQSRHLDLAVQVTEVYATYTHCCVNPVIYAVP	304		
Qy	301	GKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGSEQIESVG	351		
Db	305	GERPFRKYIROLFHRPRAVHIKKVTPFVNDPILFRVSSST-SPDSTGFRHY-SAG	354		

RESULT 5
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I49339
R/Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A/Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes
A/Reference number: I49339; MUID:95340546; PMID:7542241
A/Accession: I49339
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-355 <RES>
A/Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881547
C/Superfamily: vertebrate rhodopsin

[illegible]

QY 190 WKNFQTLKVIIGLIVPLLMVWVICYSGILKTLKRCNEKKHRAVRLIPTIMIVYFLFWA 249
 DB 195 WKRFQALKNLGLLPLLMVCIYAGIIRILLR-RPSEKKVKAURLIFAITLLFLFWT 253
 QY 250 PYNIVLLMTFQEFFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLL 309
 DB 254 PYNLSVFSVSAFDVLFTWQCEQSKHLDLQAMQVTEVIATHTCCVNPILIYVVGFRFWKYL 313
 QY 310 VVFQKHIAKFCCKCSIFQOEAPERASSVYTRTSGEQISVG 351
 DB 314 QLFQRHVAIPLAKWLPFLSVDLQERTSSI-SPSTGEHELQAG 354

RESULT 6
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I49341
 R/Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A/Title: Cloning and differential tissue-specific expression of three mouse be
 A/Reference number: I49339; MUID:95340546; PMID:7542241
 A/Accession: I49341
 A/Status: preliminary;
 A/Molecule type: DNA
 A/Residues: 1-359 <RES>
 A/Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552
 C/Superfamily: vertebrate rhodopsin

Query Match 54.5%; Score 1003.5; DB 2; Length 359;
 Best Local Similarity 56.5%; Pred. No. 9, 4e-75;
 Matches 191; Conservative 55; Mismatches 89; Indels 3; Gaps 3;

QY 14 YTTSEPCQKINVKQIAARLLPPLYSLVFIFGVGNMLVILILNCKLKSMTDIYLLNLA 73
 DB 22 YEWAPPECKVRKELGSMLLPPLYSLVFIIGLGNMVMVILIKYKRLQIMTNIYLFNLA 81
 QY 74 ISDLFPLLTPVFWAHY-LAAQNDQNTWCQLLTGLYFIFGPSGIFFFIILLTIDRYLAVH 132
 DB 82 ISDLLFLTPVFWIHYVLLMNEWFGHYCKMLSGFYILALYSEIFFIILLTIDRYLAIVH 141
 QY 133 AVFALKARTVTFGVTSVITVVAVFASLPGIIFTRSQEGLHYTCSSHFPYSQYQFWKN 192
 DB 142 AVFALRARTVTATITSIITWGLAGLALPEFIFHESQDSGFECSCPRYPEGEEDSWKR 201
 QY 193 FQTLKIVILGLVPLLMVWVICYSGILKTLKRCNEKKHRAVRLIPTIMIVYFLFWAPYN 252
 DB 202 FHAIERNVIFGLALPLLMVWVICYSGIHKTLRCPN-KKKHKAIRLIYFVMIVFFIFWTPYN 260
 QY 253 IVLLMTFQEFFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFVGEKFRNYLLVFF 312
 DB 261 LVLLPSAFHSTFLETSCEQSKHLDLQAMQVTEVIATHTCCVNPILIYVVGFRFKHLELF 320
 QY 313 QKHIAKFCCKCSIFQOEAPERASSVYTRTSGEQISV 350
 DB 321 HRNVQFTWENIFQFLPGENGRTSSV-SPSTGEQISV 357

```

RESULT 7.
G02436      chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
S;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H01272
A;Accession: G02436
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>

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A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1.; PID:g1477560
R;Combiadere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237; MUID:95348056; PMID:7622448
A;Accession: A57237
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1.; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1

C;Genetics:
A;Gene: GDB:CMKBR3
A;Cross-references: GDB:S79624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.9%; Score 936.5; DB 2; Length 355;
Best Local Similarity 53.0%; Pred. No. 2.8e-69;
Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;

Qy 20 CQINKVQIAARLLPPLYSIVTFYFGVGNMLVILINCKRLKSMTDIYLLNLAI SDLFF 79
Db 24 CERADTEALMAQFPPLYSIVFTGLGNNVVVMILLKYERLRIMINYLNLAI SDLFF 83
Qy 80 LLTVPFWAHYLA-A-QWDFGNMTCOLLTGLYPIGFSGIPPIILLTTIDRYLVAVHVPALK 138
Db 84 LVTLPEWHYVRGHNVWFHGMCKLISGFVHTGLYSEIFFIILLTTIDRYLAIVHAVFALE 143
Qy 139 ARTVTFGVTSVITWVAVFASIPGIIFTRSQEGLHYTCSSHPPYSQYQFWKNFOTLKI 198
Db 144 ARTVTFGVTSVITWGLAVLAALPEFIYFEELBETLCSDLYPEDTYSWRHFHTLM 203
Qy 199 VILGLVLPLVLMVICSGILKTLLRCNRNEKKRHRAVRLIFTIMIVFLFWAPYNIVLLN 258
Db 204 TIFCLVLPLVMAICYTGIIKTLRCP-S-KKKYKAIRLFVINA VFFIWTPTNVALLS 262
Qy 259 TFQEFGGLNCSNRLDQAMQVETLTGMTHCCINPIIYA FVGKEFRNYLLVFPQKHAK 318
Db 263 SYQSILPGNDCERTKHLDLVMLETVIAYSHCCNPVIYAFVGERFKYLRHFHRLLM 322
Qy 319 RFPKCCSI FQEQAPERASSVYTRSTGEQESV 350
Db 323 HLGRYIPFLPSEKLERITSSV-SPSTAEP ELSI 353

RESULT 8
A57160 chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; ;
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor ccr4
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAAS9743.1; PID:g9714
A;Note: source clone K5-5

C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM>
F;76-97/Domain: transmembrane #status predicted <TM>
F;112-133/Domain: transmembrane #status predicted <TM>
F;151-175/Domain: transmembrane #status predicted <TM>
F;208-226/Domain: transmembrane #status predicted <TM>
F;243-264/Domain: transmembrane #status predicted <TM>
F;291-308/Domain: transmembrane #status predicted <TM>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 49.6%; Score 914; DB 2; Length 360;
Best Local Similarity 49.6%; Pred. No. 2e-67;
Matches 175; Conservative 68; Mismatches 100; Indels 10; Gaps 6;

QY 2 DYQVSSPIYDINVTSE----PCQKINVKQIAARLLPPLYSLVPIFGVGNMLVILILIN 57
DB 8 DTLDESIIYS-NYYLYESIPKCTKEGKAFGEFLPPLYSLVFVGLGNSVVVLFX 66
QY 58 CKRLKSMTDIYLLMLAISDLFFLLTPVFWAHYLAQWDFGNMQLLTGLYFIFGRSGIF 117
DB 67 YKRLRSMTDVLLMLAISDLFFVSLFPGVGYAADQWVGLGCKMISWMLVGFYSGIF 126
QY 118 FIILLTIDRYLAVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKEGLHYT 177
DB 127 FVLMISIDRYLAIHAVFSLRARTLTGVITSLATWSVAVFASLPGLFSTCYTERNHTY 186
QY 178 CSSHPFYSQVQFNQFTLKIVILGLVPLVMVVCYSGILKTLRCNKKRRAVRLI 237
DB 187 CKTKYSLNS-TTWKVLSSLEINILGLVPLGIMLFCYSMIIRTLQHCNKK-NKAVMI 244
QY 238 FTIMIVFLFWAFNIVLLANTFOEFGNANCSNRLDQAMQVTEGLMTHCCINPIIY 297
DB 245 FAVVLFLGFWTFNIVFLETLVEVLQDCTFLERYLDVAIQATETLGFTHCCINPIY 304
QY 298 AFVGEKFRNLLVFFQKHAKRF--CKCCSIFQOEAPERASSVYTRSTGEQE 348
DB 305 FFLGKFRKYLQLF-KTCRGLFVLCYQGLLIQIYSADTPSSSYTQSTVDHDL 356

RESULT 9
JC4587
Chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
F;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g116
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: Glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 48.9%; Score 901; DB 2; Length 360;

Best Local Similarity 49.6%; Pred. No. 2.3e-66;
Matches 170; Conservative 69; Mismatches 98; Indels 6; Gaps 4;

QY 9 IYDINY--TSBPCKINVKQIAARLLPPLYSLVPIFGVGNMLVILILINCKRLKSM 65
DB 15 VINSYFYBSPKPCKEGKAFGEVFLPPLYSLVFLGFGNSVVVLVFLFKYKRLKSM 74
QY 66 DIYLLMLAISDLFFLLTPVFWAHYLAQWDFGNMQLLTGLYFIFGRSGIFFIILLTID 125
DB 75 DVYLLMLAISDLFFVSLFPGVGYAADQWVGLGCKIVSMVWLVGYSYGIFFIIMLSID 134
QY 126 RYLAVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKEGLHYTCSSHPFYS 185
DB 135 RYLAIHAVFSLKARTLTGVITSLATWSVAVFASLPGLFSTCYTERNHTYCKTQYSVN 194
QY 186 QYQFQWKNFOTLKIVILGLVPLVMVVCYSGILKTLRCNKKRRAVRLIITMIVYF 245
DB 195 S-TTWKVLSSLEINILGLVPLGIMLFCYSMIIRTLQHCNKK-NNAVRFVGVVFL 252
QY 246 LFWAPYNIVLLANTFOEFGNANCSNRLDQAMQVTEGLMTHCCINPIIYAFVGEKFR 305
DB 253 GFWTPYNNVLFLETLVEVLQDCTFLERYLDVAIQATETLGFTHCCINPIYFLGKFR 312
QY 306 NYLLVFFQKHAKR-FCKCCSIFQOEAPERASSVYTRSTGEQE 347
DB 313 KYITQLFTRCGRPLVLCCKDCFLQVYSADMSSSYTQSTVDHD 355

RESULT 10
S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S55594

R;RefSeq: E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g69517

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 45.2%; Score 832; DB 2; Length 383;

Best Local Similarity 47.4%; Pred. No. 1.1e-60;

Matches 157; Conservative 65; Mismatches 101; Indels 8; Gaps 3;

QY 11 DINYTSEPCQKINVKQIAARLLPPLYSLVPIFGVGNMLVILILINCKRLKSM 70
DB 53 DVDYESAPCYSDTTTLAAQVVPADYLLVFLGGLGNILWIIIVRYMKIKLNTMLL 112
QY 71 NLAISDLFFLLTPVFWAHYLA--QWDFGNMQLLTGLYFIFGRSGIFFIILLTIDRYL 128
DB 113 NLAISDLFFLLTPFWMHVGMVHDWTFGISLCKLRGVMSLYSQVFCIILLTVDRL 172
QY 129 AVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKEGLHYTCSSHPFYSQY 188
DB 173 AVVAVTALRFRFTVTCGIVTCVCTWFLAGLLSLPEFFHGHQDNGRVQCDPYPEMSTN 232
QY 189 FKNQFOTLKIVILGLVPLVMVVCYSGILKTLRCNKKRRAVRLIITMIVYFLEW 248
DB 233 VMRAHAVAKVIMLSLPLIMAVCYVIRRLR-RPSKKYKAIKRLIVMAYFVFW 291
QY 249 APYNIVLLANTFOEFGNANCSNRLDQAMQVTEGLMTHCCINPIIYAFVGEKFRNYL 308
DB 292 TPNIVLLSTTHATLNLQCALSSMLDALLITKIVATHTCCINPIYAFVGEKFRRL 351
QY 309 LVFFQKHAKRFCKCCSIFQ-----QEAPER 334
DB 352 YHFFHYVAIYLCKIPFLSGDGEKGPTR 382

RESULT 11

I49340
MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g88154.1; PID:g88154
C;Superfamily: vertebrate rhodopsin

Query Match 43.6%; Score 802.5; DB 2; Length 356;
Best Local Similarity 45.0%; Pred. No. 2.6e-58;
Matches 159; Conservative 69; Mismatches 118; Indels 7; Gaps 4;

QY 5 VSSPIYDI----NYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
DB 6 VTSPSYNTAKNDPMSGFLCFSINVRAGITVPTPLYSLVFIIGVGHVLLVJLQHKR 65
QY 61 LKSMTDIYLNLAISDLFFLLTVFPAHY-LAAQWDFGNMTCOLLGLYFGFSGIFFI 119
DB 66 LRNWTSYLNLALSILVFLSTLPFWVDYIMKGDWIFGNACKFVSGFYILGLYSDFE 125
QY 120 ILTIDRYLAVHVAFAKARTVTFGVVTVITWVAVFASLPGIIFTRSQEGLHYTCS 179
DB 126 TLLTIDRYLAVHVAFAKARTVTFGIISIIITWVLAALWSIPCLYVFKSQMEFTYH 185
QY 180 SHPYSQYQWKNFOTLKIVILGLVPLLVWVLCYSGILKTLRCNEKKHRAVLIFT 239
DB 186 ALLPKSLIRFLRQALTMNIGLILPLLAMIICYTRIINVLNR-RPNKKAKMRLIFV 244
QY 240 IMTVYFLFAPYINVLNLTFOQFFGLNCGSSNRLDQAMQVTTGLMTHCCINPIYAF 299
DB 245 ITLLFFLLAPYLAAPVSADFVLFTPSCLRSQOVDLSLMIETALAYTHCCVNPVY 304
QY 300 VGEKFRNVLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGBOEISVGL 352
DB 305 VGRFRKRYQLFRRHRTAILPQWLPLFSLSDRAQASA-RLPSTVEIETSD 356

RESULT 12

JC5067
G protein-coupled receptor CRK-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5067; G02776; G02387
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G proteins.
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067
A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: UNIPROT:P51685; NID:g1668735; PIDN:CAB02142.1; PID:g1668735
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996

A;Reference number: H01154

A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBR12; TER1; CRK-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 40.8%; Score 751.5; DB 2; Length 355;
Best Local Similarity 41.4%; Pred. No. 3.8e-54;
Matches 149; Conservative 66; Mismatches 124; Indels 21; Gaps 6;

QY 1 MDYQSSPIYDI-NYY----TSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMLVIL 55
DB 1 MDYTLDSLTVTVDYYPDPFISSPCDAELIQTNKLLAVFYCLLFVFLGNSLVILV 60
QY 56 INCKRLKSMTDIYLNLAISDLFFLLTVFPAHYLAAQWDFGNMTCOLLGLYFGFSG 115
DB 61 VVCKLRSITDYLNLALSDELFFVFPFYQYLLDQWVFMCKVSGFYIGFYFS 120
QY 116 IFFIILLTIDRYLAVHVAFAKARTVTFGVVTVITWVAVFASLPGIIFTRSQEGLH 175
DB 121 MFFITLMSVDRLVAVHVAVALKVRTIRMGTTLCIAVWLTAIWATIPLVFYQVASE 180
QY 176 YTCSSHPYSQYQWKNFOTLKIVILGLVPLLVWVLCYSGILKTLRCNEKKHRAVR 235
DB 181 LQCYSL-FYNQOTLKWKIFTNFMNLLGLLIPFTIFMFCYIKILHQLKRCQNHNT-KAIR 238
QY 236 LIFTIMTVYFLFAPYINVLNLTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPI 295
DB 239 LVLIVVIALFWVPFNVLFTLSHSMILDCSSISQQLTYATHVTEIISFTHCCVNPV 298
QY 296 IYAFVGEKFRNVLVFFQKHIAKFCCKCSIFQ-----QOEAPERASSVYTRSTGEOE 348
DB 299 IYAFVGEKFKHLSEIFQK-----SCSQIFNVLGRQMPRESCKSSCCQHQSSRSSV 351

RESULT 13

I58186
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g4341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 38.9%; Score 717; DB 2; Length 354;
Best Local Similarity 40.9%; Pred. No. 2.5e-51;
Matches 148; Conservative 59; Mismatches 125; Indels 30; Gaps 6;

QY 6 SSPIYDINY----TSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKRL 61

Db 4 SFPELDLENFSDSAEACYLGDIVAFGTIFLSIFSLVTFGLVGNLLVVLALTSNRKS 63
QY 62 KSMTDIYLLNLAISDLPELLTVPFWAHYLAQWDFGNMTCOLLTGLYFIFGFSIGFIIL 121
Db 64 KSITDIYLLNLAISDLFVATLPFWTHYLSHEGLHNAKCLTATPAFFIGFGGIFITV 123
QY 122 LTIDRYLAVHVAHPALKARTVTFGVTSVITWVAVFASLPFGIIFTRSQEGLHYTCS 181
Db 124 ISIDRYLAIVLAANSMNRITVQHGVTISLGVWAAAILVASPQFMFTKRDN----ECLGD 179
QY 182 FPIYQYQFNKFTLKIIVLGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIM 241
Db 180 YPEVLQBIWPLENSEVNIILGVLPLTMSFCYFRIVRTLFSCKNRKA-RAIRLILVV 238
QY 242 IVYFLFWAPYNIULLNTFOEFFGLNNSSNRLDOAMQVETLGMTHCCINPIIYAFVG 301
Db 239 VVPLFWTPYNIIVLFTLKYFNFPSCGMKDRWLALSVTETVAFSHCCINPIIYAFAG 298
QY 302 EKFRNYLLVFFQKHIAKRFCKCCSIF-----QOEAPERASSVYTRSTGRQEI 348
Db 299 EKFRNYL-----RHL-----YNNKCLAVLCGRPVHAGFSTESQSRQDSILSSILHYTSSEG 350
QY 349 SV 350
Db 351 SL 352

RESULT 14

JC4304
Orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
A;Reference number: JC4304; MUID:75011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:G665580; PIDN:AAA91783.1; PID:G665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
C;Genetics:
A;Gene: V28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 36.7%; Score 675.5; DB 2; Length 355;
Best Local Similarity 43.2%; Pred. No. 6.4e-48;
Matches 130; Conservative 55; Mismatches 111; Indels 5; Gaps 3;

QY 17 SEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKRLKSMTDIYLLNLAISD 76
Db 18 AEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVFWALTNSKPKSVTDIYLLNLAISD 77
QY 77 LPFLLTVPFWAHYLAQWDFGNMTCOLLTGLYFIFGFSIGFIILKTIDRYLAVHVA 136
Db 78 LLFVATLPFWTHYLINEKGLHNAKCTTATPAFFIGFGSIFFITVTSIDRYLAIVLAANS 137
QY 137 LKARTVTFGVTSVITWVAVFASLPFGIIFTRSQEGLHYTCSHPFPYQYQFNKFTL 196

Db 138 MNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKEN---ECLGDYDEVLQEIWPVLNRV 193
QY 197 KIVILGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIMIVYFLFWAPYNI 256
Db 194 ETNPLGFLLPILLMSYCYFRIIQTLSCKNRKA-KAIIKULLLVIVVFFLFWTPYNNWIF 252
QY 257 LNTFOEFFGLNNSSNRLDOAMQVETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKH 316
Db 253 LETLKLKYDFPPSCDMRDLRLALSVTETVAFSHCCINPLIYAFAGEFRYLYHLYGKCL 312
QY 317 A 317
Db 313 A 313

RESULT 15

JCS942
chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC5942
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <FAN>
A;Cross-references: UNIPROT:O00421; GB:U97123; NID:G2897070; PIDN:AAC39595.1; PID:G2897
C;Superfamily: vertebrate rhodopsin

Query Match 36.4%; Score 670; DB 2; Length 344;
Best Local Similarity 40.9%; Pred. No. 1.7e-47;
Matches 137; Conservative 64; Mismatches 108; Indels 26; Gaps 7;
QY 17 SEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKRLKSMTDIYLLNLAISD 76
Db 25 AEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLVLVILVKYGLKRVENIYLLNLAISN 84
QY 77 LPFLLTVPFWAHYLAQWDFGNMTCOLLTGLYFIFGFSIGFIILKTIDRYLAVH- 135
Db 85 LCPELLTLPFWAH-----AGGDPMKILIGLYFVGLYSETFFNCLLTQVQYLVFLHKG 138
QY 136 ALKARTVTFGVTSVITWVAVFASLPFGIIFTRSQEGLHYTCS-SHPFPY--SQYQFNK 192
Db 139 FSARRVPVCGIITSVLAWVTAILATLPEYVYVYKPMQEDQKYKCAFSTPPLPADETFWK 198
QY 193 FQTLKIVILGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIMIVYFLFWAPY 252
Db 199 FLTLKNNISVLVLPFLFIFYVQMKTL---RFRQRYSLFKLVFAIMVWVFLMWPYN 255
QY 253 IVLLNTFOEFFGLNNSSNRLDOAMQVETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312
Db 256 IAPFLSTFKHEFSLSDCKSYNLDKSVHITKLTATTHCCINPLLYAFLDGTFSKYL---- 311
QY 313 QKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQE 347
Db 312 -----CRCFHL-RSNTPLQPRGQSAQTSREE 337

Search completed: October 3, 2005, 07:48:34

Job time : 29 secs

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GenCore version 5.1.6
Copyright: (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 06:53:54 ; Search time 98 Seconds
(without alignments)
1839.305 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDYQVSSPIYDINYTSEPC.....ERASSVYTRSTGQEISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	1	CKR5_HUMAN
2	1830	99.4	352	1	CKR5_PANPA
3	1830	99.4	352	1	CKR5_PANTR
4	1825	99.1	352	1	CKR5_PONPA
5	1825	99.1	352	1	CKR5_PONPY
6	1825	99.1	352	2	Q71T22
7	1820	98.9	352	1	CKR5_GORGO
8	1820	98.9	352	1	CKR5_HYLSY
9	1820	98.9	352	2	Q71T20
10	1820	98.9	352	2	Q71T21
11	1818	98.8	352	2	O18771
12	1818	98.8	352	2	O18772
13	1817	98.7	352	2	Q9XS99
14	1816	98.6	352	1	CKR5_SEMEN
15	1816	98.6	352	1	CKR5_TRAPH
16	1816	98.6	352	2	Q71T26
17	1816	98.6	352	2	Q9TV50
18	1813	98.5	352	1	CKR5_HYLM
19	1812	98.4	352	2	Q95NC7
20	1811	98.4	352	1	CKR5_LOPAT
21	1811	98.4	352	1	CKR5_PAPAN
22	1811	98.4	352	1	CKR5_PAPHA
23	1811	98.4	352	2	Q95NC8
24	1811	98.4	352	2	Q95NC8
25	1811	98.4	352	2	Q71U18
26	1810	98.3	352	1	CKR5_PYGB1
27	1810	98.3	352	1	CKR5_PYGNE
28	1809	98.3	352	1	CKR5_HYLL
29	1808	98.2	352	1	CKR5_MACFA
30	1808	98.2	352	1	CKR5_MACMU
31	1808	98.2	352	1	CKR5_MACNE

32 1808 98.2 352 2 O97962
33 1808 98.2 352 2 O71T27
34 1808 98.2 352 2 O71T28
35 1808 98.2 352 2 O71T29
36 1808 98.2 352 2 Q7J34
37 1807 98.2 352 2 O95NC1
38 1807 98.2 352 2 O9XT14
39 1806 98.1 352 2 O95NC3
40 1806 98.1 352 2 O95NC6
41 1804 98.0 352 2 O9XT13
42 1803 97.9 352 2 O18770
43 1803 97.9 352 2 O9TSK1
44 1803 97.9 352 2 O9TV49
45 1802 97.9 352 2 O97975

ALIGNMENTS

RESULT 1

CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; Q9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS)
DE (HIV-1 fusion coreceptor) (CHEMR13) (CD195 antigen).
GN Name=CCRS5; Synonyms=CMKBR5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485; DOI=10.1021/bi952950g;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human CC-
chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314; DOI=10.1074/jbc.271.29.17161;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human CC
chemokine receptor (CCRS) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CCR5, a human monocyte CC
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human

RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Embrechts C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RL D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201; DOI=10.1074/jbc.272.49.30662;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
with 5'-end heterogeneity, dual promoter usage, and evidence for
polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA Magierowska M., Barre-Sinoussi F., Issefras H., Theodorou I.,
RL Debre P.;
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511; DOI=10.1038/381661a0;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RL di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of HIV-
1.";
RL Nature 381:661-666(1996).
RN [11]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512; DOI=10.1038/381667a0;
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RL Nagashima K.A., Cavanaugh C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor CC-
CR5.";
RL Nature 381:667-673(1996).
RN [12]
RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882; DOI=10.1016/S0092-8674(00)80577-2;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RL Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
entry.";
RL Cell 96:667-676(1999).
RN [13]
RP FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation. Acts as coreceptor with CD4 for primary non-
syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
virus. It promotes Env-mediated fusion of the virus.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Found in promyelocytic cell.
CC -1- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC -1- PTM: Modified by O-linked glycosylation, but not by N-linked
glycosylation.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X91492; CAA62796.1; -
DR EMBL; U54994; AAC50598.1; -
DR EMBL; U57840; AAB17071.1; -
DR EMBL; U95626; AAB57793.1; -
DR EMBL; U83326; AAC51797.1; -
DR EMBL; AF011500; AAB65700.1; -
DR EMBL; AF011501; AAB65701.1; -
DR EMBL; AF011502; AAB65702.1; -
DR EMBL; AF011503; AAB65703.1; -
DR EMBL; AF011505; AAB65705.1; -
DR EMBL; AF011506; AAB65706.1; -
DR EMBL; AF011507; AAB65707.1; -
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DR EMBL; AF011509; AAB65709.1; -
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DR EMBL; AF011511; AAB65711.1; -
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DR EMBL; AF011537; AAB65737.1; -
DR EMBL; AF031237; AAB94735.1; -
DR EMBL; AF052539; AAD18131.1; -
DR EMBL; AY221093; AAO65971.1; -
DR Genew; HGNC:1606; CCR5.
DR MIM; 601373; -
DR GO; GO:0003768; C:Endosome; TAS.
DR GO; GO:0003687; C:integral to plasma membrane; TAS.
DR GO; GO:0016493; F:C-C chemokine receptor activity; NAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; ChkRine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Sulfation;
transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).

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FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).

Query Match
Best Local Similarity 99.7%; Score 1836; DB 1; Length 352;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQDFGNTMCQLTGLYFIFGFSGIFPII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQDFGNTMCQLTGLYFIFGFSGIFPII 120
Qy 121 LLTDIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTDIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIYLLNTFOEFGLNCSNRLDQAMQVTELTGTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFOEFGLNCSNRLDQAMQVTELTGTHCCINPIIYAFV 300
Qy 301 GEKFRNLYLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNLYLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 2
CKR5 PANPA
ID CKR5 PANPA STANDARD; PRT; 352 AA.
AC P60574;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Name=CCR5; Synonyms=CMKBR5;
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9597;
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC EMBL; AF177893; AAK43376.1; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEPT_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
KW

```

```

FT TRANSMEM 1 30 Extracellular (Potential).
FT DOMAIN 31 58 1 (Potential).
FT TRANSMEM 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT TRANSMEM 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT TRANSMEM 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT TRANSMEM 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT TRANSMEM 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT TRANSMEM 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT TRANSMEM 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
FT CARBOHYD 268 268 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 40539 MW; 4A33B69880FE34C CRC64;

Query Match
Best Local Similarity 99.4%; Score 1830; DB 1; Length 352;
Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQDFGNTMCQLTGLYFIFGFSGIFPII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQDFGNTMCQLTGLYFIFGFSGIFPII 120
Qy 121 LLTDIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTDIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIYLLNTFOEFGLNCSNRLDQAMQVTELTGTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFOEFGLNCSNRLDQAMQVTELTGTHCCINPIIYAFV 300
Qy 301 GEKFRNLYLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNLYLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 3
CKR5 PANTR
ID CKR5 PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Name=CCR5; Synonyms=CMKBR5;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RP SEQUENCE FROM N.A.
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."
RT

```

RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RA "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RT AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97426118; PubMed=9282822;
 RX Zacharova V., Zachar V., Goutin A.S.;
 RA "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host.";
 RN AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98090115; PubMed=9430250;
 RX Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RA "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RT AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RN SEQUENCE FROM N.A.
 RP Zhang Y., Ryder O.A., Zhang Y.;
 RA "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RN Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF005663; AAB62557.1; -;
 DR EMBL; U94329; AAB58446.1; -;
 DR EMBL; AF011542; AAB65742.1; -;
 DR EMBL; U97666; AAC51670.1; -;
 DR EMBL; AF011540; AAB65740.1; -;
 DR EMBL; U89797; AAC03717.1; -;
 DR EMBL; AF177894; AAK43377.1; -;
 DR InterPro; IPR002240; CC 5 receptor.
 DR InterPro; IPR000355; Chkine_receptor.
 DR InterPro; IPR002276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
 KM G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
 FT DOMAIN 1 30
 FT Extracellular (Potential).
 FT TRANSMEM 31 58
 FT 1 (Potential).
 FT DOMAIN 59 68
 FT Cytoplasmic (Potential).
 FT TRANSMEM 69 89
 FT 2 (Potential).
 FT DOMAIN 90 102
 FT Extracellular (Potential).
 FT TRANSMEM 103 124
 FT 3 (Potential).
 FT DOMAIN 125 141
 FT Cytoplasmic (Potential).
 FT TRANSMEM 142 166
 FT 4 (Potential).
 FT DOMAIN 167 198
 FT Extracellular (Potential).
 FT TRANSMEM 199 218
 FT 5 (Potential).
 FT DOMAIN 219 235
 FT Cytoplasmic (Potential).

FT TRANSMEM 236 260 6 (Potential).
 FT DOMAIN 261 277 Extracellular (Potential).
 FT TRANSMEM 278 301 7 (Potential).
 FT DOMAIN 302 352 Cytoplasmic (Potential).
 FT DISULFID 101 178 By similarity.
 FT MOD_RES 3 3 Sulfotyrosine (By similarity).
 FT MOD_RES 10 10 Sulfotyrosine (By similarity).
 FT MOD_RES 14 14 Sulfotyrosine (By similarity).
 FT MOD_RES 15 15 Sulfotyrosine (By similarity).
 FT CARBOHYD 268 268 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 123 123 T -> S (in Ref. 1).
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;
 Query Match 99.4%; Score 1830; DB 1; Length 352;
 Best Local Similarity 99.1%; Pred. No. 9.8e-105;
 Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQSSPIYDINYITSEPCQKINVKQIAARLLPPLYSLVFVFGVGNMLVILLINCKR 60
 DB |||||
 DB 1 MDYQSSPIYDIDYITSEPCQKINVKQIAARLLPPLYSLVFVFGVGNMLVILLINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
 DB |||||
 DB 61 LKSMTDIYLLNLAIISDLFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
 QY 121 LLTDIRYLAHVHAFKARTVTGVTSTVITWVAVFASLPGIITRQKQGLHYTCSS 180
 DB |||||
 DB 121 LLTDIRYLAHVHAFKARTVTGVTSTVITWVAVFASLPGIITRQKQGLHYTCSS 180
 QY 181 HPFYSQYQFQKFNQFQTLKIVILGLVPLLVWVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
 DB |||||
 DB 181 HPFYSQYQFQKFNQFQTLKIVILGLVPLLVWVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
 QY 241 MIVYFLWAPYXIVILLNTFQBFGLNCCSSNRLDQAMQVTTETLGMTHCCINPIIYAFV 300
 DB |||||
 DB 241 MIVYFLWAPYXIVILLNTFQBFGLNCCSSNRLDQAMQVTTETLGMTHCCINPIIYAFV 300
 QY 301 GKFRNYLLVFPQKHIAKRFCCCSIFQOEAPERASSVYTRSTGEQIEISVGL 352
 DB |||||
 DB 301 GKFRNYLLVFPQKHIAKRFCCCSIFQOEAPERASSVYTRSTGEQIEISVGL 352
 RESULT 4
 ID CCR5_PONPA STANDARD; PRT; 352 AA.
 AC F61756;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CR-5) (CCR-5) (CCR5).
 GN Name=CCR5; Synonyms=CMGR5;
 OS Pongo pygmaeus abelii (Sumatran orangutan).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9601;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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EMBL; AF177895; AAK43378.1; -
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 FT CARBOHYD 268 268
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 99.1%; Score 1825; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 2e-104;
 Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPTDYDINTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPTDYDINTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
 Qy 61 LKSMTDIYLLNLAISSDLFELLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
 Db 61 LKSMTDIYLLNLAISSDLFELLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
 Qy 121 LLTIDRYLAVHVAFAFKARTVTGVTSTVITWVAVFASLPGLIFTRSQKGLHYTCSS 180
 Db 121 LLTIDRYLAVHVAFAFKARTVTGVTSTVITWVAVFASLPGLIFTRSQKGLHYTCSS 180
 Qy 181 HPFYSQYQFWKPFOTLKIVILGLVPLLVVVICYSGLKTLKLLCRNEKKHRAVRLIFTI 240
 Db 181 HPFYSQYQFWKPFOTLKIVILGLVPLLVVVICYSGLKTLKLLCRNEKKHRAVRLIFTI 240
 Qy 241 MIVVLEFWAPNIVLLNTQEPFGNLCSSNRLDQAMQVTELTGTHCCINPIIYAFV 300
 Db 241 MIVVLEFWAPNIVLLNTQEPFGNLCSSNRLDQAMQVTELTGTHCCINPIIYAFV 300
 Qy 301 GEKFRNLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQISVGL 352

RESULT 5

CKR5_PONPY STANDARD; PRT; 352 AA.
 AC 097881;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN Name=CCR5; Synonyms=CNKR5;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_Taxid=9600;

RN SEQUENCE FROM N.A.
 RP MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC EMBL; AF075446; AAD19858.1; -
 DR InterPro; IPR002240; CC 5 receptor.
 DR InterPro; IPR000355; Chkline receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 99.1%; Score 1825; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 2e-104;
 Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDYQVSSPTDYDINTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPTDYDINTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
 Qy 61 LKSMTDIYLLNLAISSDLFELLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
 Db 61 LKSMTDIYLLNLAISSDLFELLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
 Qy 121 LLTIDRYLAVHVAFAFKARTVTGVTSTVITWVAVFASLPGLIFTRSQKGLHYTCSS 180
 Db 121 LLTIDRYLAVHVAFAFKARTVTGVTSTVITWVAVFASLPGLIFTRSQKGLHYTCSS 180
 Qy 181 HPFYSQYQFWKPFOTLKIVILGLVPLLVVVICYSGLKTLKLLCRNEKKHRAVRLIFTI 240
 Db 181 HPFYSQYQFWKPFOTLKIVILGLVPLLVVVICYSGLKTLKLLCRNEKKHRAVRLIFTI 240

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QY 241 MIVYFLWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352

RESULT 6
Q71IT22
ID Q71IT22 PRELIMINARY; PRT; 352 AA.
AC Q71IT22
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE C-C chemokine receptor 5.
GN Name=CCR5;
OS Pongo pygmaeus pygmaeus (Bornean orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9602;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177900; AAK43383.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signal. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPT FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 99.1%; Score 1825; DB 2; Length 352;
Best Local Similarity 98.9%; Pred. No. 2e-104;
Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPTIDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFGNMLVILINCKR 60
Db 1 MDYQVSSPTIDIDYTTSEPCQKINVKQIAARLLPPLYSLVIFGFGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALSIDFLFTLLTPVFAHYLAQWDFGNTWCQLLTGLYFTGFSGFFII 120
Db 61 LKSMTDIYLLNLALSIDFLFTLLTPVFAHYLAQWDFGNTWCQLLTGLYFTGFSGFFII 120
QY 121 LLATIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLATIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPFYQSQVQWKNFOTLKIVILGLVPLLVVVIYCYSGILKTLKCRNEKKHRAVRLIFTI 240
Db 181 HPFYQSQVQWKNFOTLKIVILGLVPLLVVVIYCYSGILKTLKCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHAKRCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352

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RESULT 7
CKR5_GORGO
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Name=CCR5; Synonyms=CMKBR5;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharzon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Feilner S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC -----
CC EMBL; AF062553.1; -.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPT FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT FL 2; 1.
DR G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
KW DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT DOMAIN 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 Cytoplasmic (Potential).
FT DOMAIN 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 98.9%; Score 1820; DB 1; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;

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Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFGVGNMLVILILINCKR 60
 Db 1 MDYQVSSPTDYDITYTSEPCKINVKQIAARLLPPLYSLVFIFGVGNMLVILILINCKR 60

Qy 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFPII 120
 Db 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFPII 120

Qy 121 LLTIDRYLVAVHVPFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 Db 121 LLTIDRYLVAVHVPFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180

Qy 181 HFPYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKGRHRAVRLIFTI 240
 Db 181 HFPYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKGRHRAVRLIFTI 240

Qy 241 MIVYFLFWAPYNIIVLLNTFOEFFGLNCSNRLDQAMQVETGLMTHCCINPIIYAFV 300
 Db 241 MIVYFLFWAPYNIIVLLNTFOEFFGLNCSNRLDQAMQVETGLMTHCCINPIIYAFV 300

Qy 301 GEKFRNVLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNVLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 8

CKRS_HYLSY
 ID CKRS_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NCS;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
 GN Name=CCRS; Synonyms=CMKBR5;
 OS Hylobates syndactylus (Siayang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF177894; AAK43367.1; -.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Cmkline_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
 FT DOMAIN 1 30 Extracellular (Potential).
 FT TRANSMEM 31 58 1 (Potential).

FT DOMAIN 59 68 Cytoplasmic (Potential).
 FT TRANSMEM 69 89 2 (Potential).
 FT DOMAIN 90 102 Extracellular (Potential).
 FT TRANSMEM 103 124 3 (Potential).
 FT DOMAIN 125 141 Cytoplasmic (Potential).
 FT TRANSMEM 142 166 4 (Potential).
 FT DOMAIN 167 198 Extracellular (Potential).
 FT TRANSMEM 199 218 5 (Potential).
 FT DOMAIN 219 235 Cytoplasmic (Potential).
 FT TRANSMEM 236 260 6 (Potential).
 FT DOMAIN 261 277 Extracellular (Potential).
 FT TRANSMEM 278 301 7 (Potential).
 FT DOMAIN 302 352 Cytoplasmic (Potential).
 FT DISULFID 101 178 By similarity.
 FT MOD_RES 3 3 Sulfotyrosine (By similarity).
 FT MOD_RES 10 10 Sulfotyrosine (By similarity).
 FT MOD_RES 14 14 Sulfotyrosine (By similarity).
 SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 98.9%; Score 1820; DB 1; Length 352;
 Best Local Similarity 98.6%; Pred. No. 4e-104;
 Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFGVGNMLVILILINCKR 60
 Db 1 MDYQVSSPTDYDITYTSEPCKINVKQIAARLLPPLYSLVFIFGVGNMLVILILINCKR 60

Qy 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFPII 120
 Db 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFPII 120

Qy 121 LLTIDRYLVAVHVPFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 Db 121 LLTIDRYLVAVHVPFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180

Qy 181 HFPYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKGRHRAVRLIFTI 240
 Db 181 HFPYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKGRHRAVRLIFTI 240

Qy 241 MIVYFLFWAPYNIIVLLNTFOEFFGLNCSNRLDQAMQVETGLMTHCCINPIIYAFV 300
 Db 241 MIVYFLFWAPYNIIVLLNTFOEFFGLNCSNRLDQAMQVETGLMTHCCINPIIYAFV 300

Qy 301 GEKFRNVLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNVLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 9

Q71TZ0
 ID Q71TZ0 PRELIMINARY; PRT; 352 AA.
 AC Q71TZ0;
 DT 03-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE C-C chemokine receptor 5.
 GN Name=CCRS;
 OS Gorilla gorilla beringei (Mountain gorilla) (Highland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9594;
 [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF177903; AAK43366.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.


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DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;

Query Match 98.9%; Score 1820; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDQVSSPTDYDYYTSEPCKTNVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGFSGIFFII 120
DB 61 LKSMTDIYLLNLAISDLFLLTPFWAHYAAAQWDFGNMTCQLLTGLYIFGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVFGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB 121 LLTIDRYLAIHVAFAKARTVFGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
QY 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKKHRAVRLIFTI 240
DB 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYINVLNTQEFPGNLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYINVLNTQEFPGNLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 10
Q71TZY PRELIMINARY; PRT; 352 AA.
AC Q71TZY; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE C-C chemokine receptor 5.
GN Name=CCRS;
OS Gorilla gorilla graueri (Eastern lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OC NCBI_TaxID=46359;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177902; AAK43385.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;
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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;

Query Match 98.9%; Score 1820; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDQVSSPTDYDYYTSEPCKTNVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGFSGIFFII 120
DB 61 LKSMTDIYLLNLAISDLFLLTPFWAHYAAAQWDFGNMTCQLLTGLYIFGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVFGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB 121 LLTIDRYLAIHVAFAKARTVFGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
QY 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKKHRAVRLIFTI 240
DB 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYINVLNTQEFPGNLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYINVLNTQEFPGNLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 11
O18771 PRELIMINARY; PRT; 352 AA.
ID O18771; 1998 (TrEMBLrel. 05, Created)
AC O18771; 1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCR5 receptor (Fragment).
GN Name=CCRS;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359564;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism. .;
RT AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF011539; AAB65739.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW NON_TER 352
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SQ SEQUENCE 352 AA; 40466 MW; 3FFAC7ABAE1D4FB CRC64;
Query Match 98.8%; Score 1818; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 5.3e-104;
Matches 347; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQWDFGNTMCOLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQWDFGNTMCOLLTGLYFIFGFSGIFPII 120
QY 121 LLTIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPYYSQVQFWKNTKIVILGLVPLLVVVICYSGLIKTLRCRNEKKRHRAVRLIFTI 240
DB 181 HPYYSQVQFWKNTKIVILGLVPLLVVVICYSGLIKTLRCRNEKKRHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIYLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQBIISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQBIISVGL 352

RESULT 12
O18772 PRELIMINARY; PRT; 352 AA.
AC O18772;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCR5 receptor (Fragment).
GN Name=CCR5;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
[1]
RN MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
SEQUENCE FROM N.A.
RX HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF011541; AAB65741.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chkine_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 352
SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 99.8%; Score 1818; DB 2; Length 352;

Best Local Similarity 98.6%; Pred. No. 5.3e-104;
Matches 347; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQWDFGNTMCOLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQWDFGNTMCOLLTGLYFIFGFSGIFPII 120
QY 121 LLTIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPYYSQVQFWKNTKIVILGLVPLLVVVICYSGLIKTLRCRNEKKRHRAVRLIFTI 240
DB 181 HPYYSQVQFWKNTKIVILGLVPLLVVVICYSGLIKTLRCRNEKKRHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIYLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQBIISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQEQAPERASSVYTRSTGEQBIISVGL 352

RESULT 13
Q9XS99 PRELIMINARY; PRT; 352 AA.
AC Q9XS99;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CC chemokine receptor 5.
GN Name=ccr5;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
[1]
RN MEDLINE=99210133; PubMed=10195758; DOI=10.1089/08922299311231;
RA Saksena N.K., Wang B., Novembre P.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF105291; AAD20560.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chkine_receptor.
DR InterPro; IPR002276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 98.7%; Score 1817; DB 2; Length 352;
Best Local Similarity 98.3%; Pred. No. 6.1e-104;
Matches 346; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60

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Db 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFGFGNMLVILILNCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGSIFII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGSIFII 120
Qy 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIITRQKGLHYTCSS 180
Db 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIITRQKGLHYTCSS 180
Qy 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Qy 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 14
CKR5 SEMEN STANDARD; PRT; 352 AA.
AC P61757;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5) .
GN Name=CCR5; Synonyms=CMKBR5;
OS Semnophthecus entellus (Hanuman langur) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Semnophthecus.
OX NCBI_TaxID=88029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC -----
DR EMBL; AF177896; AAK43379.1; -
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; GPCRs; GPCR; Sulfation; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).

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FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT DOMAIN 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT DOMAIN 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
FT CARBOHYD 268 268 N-linked (GlcNAc-) (Potential).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 98.6%; Score 1816; DB 1; Length 352;
Best Local Similarity 97.7%; Pred. No. 7e-104;
Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFGFGNMLVILILNCKR 60
Db 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFGFGNMLVILILNCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGSIFII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGSIFII 120
Qy 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIITRQKGLHYTCSS 180
Db 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIITRQKGLHYTCSS 180
Qy 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Qy 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 15
CKR5 TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5) .
GN Name=CCR5; Synonyms=CMKBR5;
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC -----

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EMBL; AF075443; AAD19855.1; -
DR InterPro; IPR002240; CC 5. receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
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FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938f CRC64;

Query Match 98.6%; Score 1816; DB 1; Length 352;
Best Local Similarity 97.7%; Pred. No. 7e-104;
Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYTSEPCKINVKQIAARLLPPLSLVFIQFVGNMVLVILINCKR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MDYQVSSPTDIDYITSEPCKQNVKQIAARLLPPLSLVFIQFVGNIILVILINCKR 60
Qy 61 LKSMTDIYLLNLALSDFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIFGFSGIFFI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 LKSMTDIYLLNLALSDFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIFGFSGIFFI 120
Qy 121 LLTIDRYLVAVHVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 LLTIDRYLVAVHVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Qy 181 HPPYSQYQFKNQFTLKIIVLGLVPLLVMI CYSGILKTLRCRNEKKRHVRLIFTI 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 HPPYSQYQFKNQFTLKIIVLGLVPLLVMI CYSGILKTLRCRNEKKRHVRLIFTI 240
Qy 241 MIVVFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
241 MIVVFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
Qy 301 GEKFRNLLVFFQKHAKRFCKCSIFQEQAPERASSVYTRSTGEQEISVGL 352
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 GEKFRNLLVFFQKHAKRFCKCSIFQEQAPERASSVYTRSTGEQEISVGL 352

Search completed: October 3, 2005, 07:45:50
Job time : 100 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 06:08:13 ; Search time 90 Seconds
(without alignments)
1512.663 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
Sequence: 1 MDVQSSPIVDINYTSSEPC.....ERASSVYRSTGQEIISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	100.0	371	2 AAW23834	Aaw23834 Human CC
2	1836	99.7	352	2 AAW27407	Aaw27407 Human CCR
3	1836	99.7	352	2 AAW27123	Aaw27123 Human che
4	1836	99.7	352	2 AAW23835	Aaw23835 Human CC
5	1836	99.7	352	2 AAW88232	Aaw88232 HIV-1 co-
6	1836	99.7	352	4 AAG80111	Aag80111 Human CCR
7	1836	99.7	352	4 AAE04321	Aae04321 Human che
8	1836	99.7	352	4 AAB83354	Aab83354 Human CCR
9	1836	99.7	352	4 AAB82948	Aab82948 Human HIV
10	1836	99.7	352	5 AAM52828	Aam52828 Human CC
11	1836	99.7	352	5 ABB08343	Abb08343 Human che
12	1836	99.7	352	6 ABR58602	Abr58602 Human can
13	1836	99.7	352	6 AAO29514	Aao29514 Human C-C
14	1836	99.7	352	6 ABP97728	Abp97728 Amino aci
15	1836	99.7	352	6 ABB81933	Abb81933 Human C-C
16	1836	99.7	352	7 ADC03341	Adc03341 Human che
17	1836	99.7	352	7 ADF44882	Adf44882 Human CC
18	1836	99.7	352	7 ADK17356	Adk17356 Human CCR
19	1836	99.7	352	7 ADP65192	Adp65192 Human che
20	1836	99.7	352	8 ADG42778	Adg42778 Human CC
21	1836	99.7	352	8 ADH60807	Adh60807 Human CC-
22	1836	99.7	352	8 ADM35887	Adm35887 Human che
23	1836	99.7	352	8 ADO29227	Ado29227 Human GPC
24	1836	99.7	352	8 ADP12403	Adp12403 Protein e
25	1836	99.7	352	8 ADO19578	Ado19578 Human PRO

26	1836	99.7	352	8 ADQ21275	Adq21275 Human sof
27	1836	99.7	352	8 ADP24004	Adp24004 PRO polyp
28	1836	99.7	352	8 ADT90847	Adt90847 Human che
29	1836	99.7	439	2 AAY41280	Aay41280 Fusion pr
30	1833	99.6	363	8 ADR88809	Adr88809 Human G p
31	1830	99.4	352	4 ABB56342	Abb56342 Non-endog
32	1830	99.4	352	5 AAM52829	Aam52829 Human CCR
33	1828	99.3	352	4 AAE07048	Aae07048 Human G-p
34	1828	99.3	352	4 AAE07039	Aae07039 Human G-p
35	1828	99.3	352	4 AAB46858	Aab46858 Human HDG
36	1828	99.3	352	5 AAU97152	Aau97152 Human G-p
37	1828	99.3	352	5 ABG70597	Abg70597 Human G-p
38	1828	99.3	352	5 ABG92883	Abg92883 Human imm
39	1828	99.3	352	5 AAE25811	Aae25811 Human G-p
40	1828	99.3	352	5 ABB81054	Abb81054 G-protein
41	1828	99.3	352	6 ABG75540	Abg75540 Human G-p
42	1828	99.3	352	6 ABU61654	Abu61654 Human G-p
43	1828	99.3	352	7 ADF72142	Adf72142 Human G-p
44	1828	99.3	352	8 ADP86210	Adp86210 Human G-p
45	1828	99.3	352	8 ADL16259	Adl16259 Human G-p

ALIGNMENTS

RESULT 1
AAW23834
ID AAW23834 standard; protein; 371 AA.
XX AC AAW23834;
XX DT 08-JUN-1998 (first entry)
XX DE Human CC chemokine receptor 5 (CCR5) A127V variant.
XX KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Domain 48..74
FT /label= I
FT /note= "transmembrane domain"
FT Domain 123..145
FT /label= III
FT /note= "transmembrane domain"
FT Domain 162..190
FT /label= IV
FT /note= "transmembrane domain"
FT Domain 213..238
FT /label= V
FT /note= "transmembrane domain"
FT Domain 257..277
FT /label= VI
FT /note= "transmembrane domain"
FT Domain 296..319
FT /label= VII
FT /note= "transmembrane domain"
WO9745543-A2.
04-DEC-1997.
28-MAY-1997; 97WO-US009586.
28-MAY-1996; 96US-0018508P.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
Broder CC, Kennedy PE;
XX

DR WPI; 1998-032650/03.
 DR N-PSDB; AAT76919.
 XX
 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 XX
 PS Example 1; Fig 1B; 70pp; English.
 XX
 CC This protein sequence comprises an Alal27Leu variant of a novel human
 CC macrophage-selective CC chemokine receptor (see also AAW23835) that has
 CC been designated CCR5. The sequence was deduced from an isolated cDNA
 CC clone (see AAT76919). The conservative variation should not affect the
 CC activity of CCR5. The susceptibility of human macrophages to HIV
 CC infection depends on cell surface expression of CD4 and CCR5. CCR5 is a
 CC member of the 7-transmembrane superfamily of G-protein coupled cell
 CC surface molecules. It plays an essential role in the membrane fusion step
 CC of infection by some HIV isolates. The establishment of stable, non-human
 CC cell lines and transgenic mammals having cells that coexpress human CD4
 CC and CCR5 provides valuable tools for research of HIV infection.
 CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents
 CC capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 CC
 XX Sequence 371 AA;
 SQ
 Query Match 100.0%; Score 1841; DB 2; Length 371;
 Best Local Similarity 100.0%; Pred. No. 9.3e-195;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILILINCKR 60
 DB 20 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILILINCKR 79
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFI 120
 DB 80 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFI 139
 QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 DB 140 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 199
 QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKRRHRAVLIFTI 240
 DB 200 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKRRHRAVLIFTI 259
 QY 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 DB 260 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 319
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352
 DB 320 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 371
 RESULT 2
 AAW27407
 ID AAW27407 standard; protein; 352 AA.
 XX
 AC AAW27407;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human CCR5.
 XX
 KW Humah Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX
 OS Homo sapiens.
 XX

PN WO9732019-A2.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-BE0000023.
 XX
 PR 01-MAR-1996; 96EP-008700021.
 PR 06-AUG-1996; 96EP-00870102.
 XX
 PA (EURO-) EUROSREEN SA.
 XX
 PI Samson M, Parmentier M, Vassart G, Libert F;
 XX WPI; 1997-479829/44.
 DR N-PSDB; AAT90117.
 XX
 PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX
 PS Claim 4; Fig 1b-c; 94pp; English.
 XX
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, alpha
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX
 SQ Sequence 352 AA;
 Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFI 120
 DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFI 120
 QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKRRHRAVLIFTI 240
 DB 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKRRHRAVLIFTI 240
 QY 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352
 DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352
 RESULT 3
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX
 AC AAW27123;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.
 XX Homo sapiens.
 XX Key: Location/Qualifiers
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 FT Domain /label= Extracellular_domain
 FT 56.67
 FT Domain /label= Intracellular_domain
 FT 89.112
 FT Domain /label= Extracellular_domain
 FT 125.145
 FT Domain /label= Intracellular_domain
 FT 166.191
 FT Domain /label= Extracellular_domain
 FT 213.235
 FT Domain /label= Intracellular_domain
 FT 259.280
 FT Domain /label= Extracellular_domain
 FT 301.352
 FT Domain /label= Intracellular_domain
 XX WO9722698-A2.
 XX 26-JUN-1997.
 XX 20-DEC-1996; 96WO-US020759.
 XX 20-DEC-1995; 95US-00575967.
 XX 07-JUN-1996; 96US-00661393.
 XX (ICOS-) ICOS CORP.
 XX Gray PW, Schweickart VL, Raport CJ;
 PI WPI; 1997-341689/31.
 DR N-PSDB; AAT85161.
 XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 FT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 FT tumours, viral infections, auto-immune diseases, etc.
 XX Claim 16; Page 47-48; 65pp; English.
 XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX Sequence 352 AA;
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 Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 MDYQVSSPIVDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHAAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
 DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITVWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITVWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 QY 181 HPFYSQYQFWKNFQTLKIVILGLVPLLVNVCISYGLKTLRCRNEKKRHRAVRLFTI 240
 DB 181 HPFYSQYQFWKNFQTLKIVILGLVPLLVNVCISYGLKTLRCRNEKKRHRAVRLFTI 240
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 DB 241 MIVYFLFWAPYNIYLLNTFQEFPGNLCSSNRLDQAMQVTTGLMTHCCINPIIVAFV 300
 QY 301 GEKFRNVLVFFQKHIAKRFCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
 DB 301 GEKFRNVLVFFQKHIAKRFCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
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 AAW23835
 ID AAW23835 standard; protein; 352 AA.
 XX AC AAW23835;
 XX 08-JUN-1998 (first entry)
 XX Human CC chemokine receptor 5 (CCR5).
 XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
 XX Homo sapiens.
 XX Key Location/Qualifiers
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 FT Domain /label= I
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 FT 104.126
 FT Domain /label= III
 FT /note= "transmembrane domain"
 FT 109.120
 FT Region /note= "extracellular loop-1 (Claim 19)"
 FT 143.171
 FT Domain /label= IV
 FT /note= "transmembrane domain"
 FT 187.210
 FT Region /note= "extracellular loop-2 (Claim 19)"
 FT 194.219
 FT Domain /label= V
 FT /note= "transmembrane domain"
 FT 238.258
 FT Domain /label= VI
 FT /note= "transmembrane domain"
 FT 261.276
 FT Region /note= "extracellular loop-3 (Claim 19)"
 FT 277.300
 FT Domain /label= VII
 FT /note= "transmembrane domain"
 XX WO9745543-A2.
 XX 04-DEC-1997.
 XX 28-MAY-1997; 97WO-US009586.
 XX 28-MAY-1996; 96US-0018508P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
 PI Broder CC, Kennedy PE;

XX WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 CC CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 FT
 XX
 PS
 XX Claim 68; Fig 1C; 70pp; English.
 XX
 CC This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYIFGFSGIFFTI 120
 Db 61 LKSMTDIYLLNLAISDLFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYIFGFSGIFFTI 120
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 Db 121 LLTIDRYLAVVHAFAVFAKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQVQFQWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
 Db 181 HPFYSQVQFQWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
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 Db 241 MIVYFLWAPYNIYLLNTQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 QY 301 GEKFRNYLLVFFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
 Db 301 GEKFRNYLLVFFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 5
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE HIV-1 co-receptor CCR5.
 XX
 KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT

FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT 103..124
 FT /note= "transmembrane domain 3"
 FT 142..167
 FT /note= "transmembrane domain 4"
 FT 200..223
 FT /note= "transmembrane domain 5"
 FT 236..260
 FT /note= "transmembrane domain 6"
 FT 275..301
 FT /note= "transmembrane domain 7"
 XX
 XX WO9854317-A1.
 PN
 XX
 XX 03-DEC-1998.
 PD
 XX
 XX 29-MAY-1998; 98WO-BP003437.
 PF
 XX
 XX 30-MAY-1997; 97US-0048057P.
 PR
 XX
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA
 XX
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI
 XX
 XX WPI; 1999-059835/05.
 DR
 XX
 XX N-PSDB; AAV84126.
 DR
 XX
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 FT
 XX
 XX Disclosure; Page 34-35; 55pp; English.
 PS
 XX
 XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW88231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 XX
 XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYIFGFSGIFFTI 120
 Db 61 LKSMTDIYLLNLAISDLFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYIFGFSGIFFTI 120
 QY 121 LLTIDRYLAVVHAFAVFAKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 Db 121 LLTIDRYLAVVHAFAVFAKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQVQFQWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
 Db 181 HPFYSQVQFQWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240

Db 181 HPPYQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 Qy 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQIBISVGL 352
 Db 301 GEKFRNYLLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQIBISVGL 352

RESULT 6
 AAG80111
 ID AAG80111 standard; protein; 352 AA.
 XX AC AAG80111;
 XX DE Human CCR5 protein.
 XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX OS Homo sapiens.
 XX FN WO200172830-A2.
 XX PD 04-OCT-2001.
 XX PF 02-APR-2001; 2001WO-EP003708.
 XX PR 31-MAR-2000; 2000DE-01016013.
 XX PA (IPFP-) IPF PHARM GMBH.
 XX PA (FORS/) FORSMANN U.
 XX PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
 XX WPI; 2001-626256/72.
 XX DR Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX PS Disclosure; Page 10; 26pp; German.
 XX CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

SQ Sequence 352 AA;

Query Match 59.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 59.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIIFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIIFGVGNMLVILINCKR 60
 Qy 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIPIII 120
 Db 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIPIII 120
 Qy 121 LLTIIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 Db 121 LLTIIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 Qy 181 HFPYSQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 Db 181 HFPYSQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 Qy 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQIBISVGL 352
 Db 301 GEKFRNYLLVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQIBISVGL 352

RESULT 7
 AAE04321
 ID AAE04321 standard; protein; 352 AA.
 XX AC AAE04321;
 XX DT 04-SEP-2001 (first entry)
 XX DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.
 XX KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR-5; envelope glycoprotein; anti-HIV.
 XX OS Homo sapiens.
 XX PN US6258527-B1.
 XX PD 10-JUL-2001.
 XX PF 21-MAY-1997; 97US-00861105.
 XX PR 20-MAY-1996; 96US-0017157P.
 XX PR 19-JUN-1996; 96US-0020043P.
 XX PR 19-MAY-1997; 97US-00858660.
 XX PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX (UUNY) UNIV NEW YORK STATE.
 XX PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
 XX WPI; 2001-417127/44.
 XX DR N-PSDB; AAD08577.
 XX PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 XX HIV.
 XX PS Disclosure; Col 47-50; 37pp; English.
 XX CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of

CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFFGVGNMLVILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFII 120
 DB 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFII 120
 QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 DB 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
 DB 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
 QY 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
 DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 8
 AAB83354
 ID AAB83354 standard; protein; 352 AA.
 XX
 AC AAB83354;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human CCR5 protein sequence.
 XX
 KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX
 OS Homo sapiens.
 XX
 PN EPI1118858-A2.
 XX
 PD 25-JUL-2001.
 XX
 PF 03-JAN-2001; 2001EP-00300020.
 XX
 PR 12-JAN-2000; 2000GB-00000659.
 PR 12-JAN-2000; 2000GB-00000661.
 PR 12-JAN-2000; 2000GB-00000663.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 XX Dobbs S, Perros M, Rickett GA;
 XX
 DR WPI; 2001-477088/52.
 DR N-PSDB; AAF87099.
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises

PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX
 PS Claim 1; Page 110; 113pp; English.
 XX

CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFFGVGNMLVILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFII 120
 DB 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFGFSGIFII 120
 QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 DB 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
 DB 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
 QY 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
 DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 9
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 XX
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Human HIV-1 co-receptor CCR5.
 XX
 KW CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 XX
 PN WO200164710-A2.
 XX

PD 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US006699.
XX 29-FEB-2000; 2000US-0185667P.
PR 19-MAY-2000; 2000US-0205839P.
PR 07-FEB-2001; 2001US-0267231P.
XX (PROG-) PROGENICS PHARM INC.
PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX Dragic T, Olson WC;
XX WPI; 2001-611273/70.
DR N-PSDB; AAH26903.
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
PT receptor) amino terminal domain including negatively charged and two
PT sulfated tyrosine residues is useful for treating HIV infection in
PT humans.
XX Claim 1; Page 30; 163pp; English.
PS The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
XX 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
CC site that determines the specificity of the interaction between CCR5 and
CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
CC CCR5 N-terminus is required for gp120 binding and may critically modulate
CC the susceptibility of target cells to HIV-1 infection in vivo. The
CC invention provides claimed sulfated peptides (see AAB82947) that are
CC based on the CCR5 N-terminal region and which are effective for
CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
CC cells from becoming infected with HIV, of treating a subject whose CD4+
CC cells are infected with HIV, and of identifying an agent which inhibits
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
CC out in a subject, especially a human, infected (therapeutic method), not
CC infected with HIV (prophylactic method), or in a subject who is not
XX infected with, but has been exposed to, HIV
XX
SQ Sequence 352 AA;
Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTGVTVTWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFFALKARTVTGVTVTWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HFPYSQFQWKNFOTLKIIVLGLVPLLLVMVICYSGILKTLRCNKKRRAVRLIFTI 240
DB 181 HFPYSQFQWKNFOTLKIIVLGLVPLLLVMVICYSGILKTLRCNKKRRAVRLIFTI 240
QY 241 MIVYFLFWAPNIVILLANTQEPFGLNCSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPNIVILLANTQEPFGLNCSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHAKRCKCSIFQQAPEPERSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHAKRCKCSIFQQAPEPERSVYTRSTGEQISVGL 352

RESULT 10
AAM52828

ID AAM52828 standard; protein; 352 AA.
XX AAM52828;
XX 22-FEB-2002 (first entry)
XX Human CC chemokine receptor 5 (CCR5).
XX CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification.
XX Homo sapiens.
OS WO200171346-A2.
PN 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009155.
XX 21-MAR-2000; 2000US-0190946P.
PR 21-MAR-2000; 2000US-0190996P.
PR 21-MAR-2000; 2000US-0191299P.
PR 20-MAR-2001; 2001US-00813448.
PR 20-MAR-2001; 2001US-00813651.
PR 20-MAR-2001; 2001US-00813653.
XX (CONS-) CONSENSUS PHARM INC.
PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
PI WPI; 2002-010610/01.
XX N-PSDB; ABA02317.
DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT comprises binding a molecule from library to a molecule having binding
PT property corresponding to CCR5 and identifying bound molecule.
XX Example 3; Fig 4A; 50pp; English.
PS
XX The invention relates to a method for identifying a binding compound for
CC chemokine receptor 5 (CCR5). The method involves screening a library
CC of test molecules (particularly peptides) with immobilised CCR5, and then
CC identifying those molecules which bind. The invention also relates to
CC CCR5-binding molecules identified using the method of the invention, a
CC methods for identifying consensus motifs for CCR5-binding peptides, a
CC transfer vector encoding tagged CCR5, a computer-aided methods for
CC determining the relative binding affinity of a test molecule to CCR5 and
CC a computer aided drug screening assay that utilises the three-dimensional
CC structure of CCR5. Compounds identified using the methods of the
CC invention are useful for treating or preventing HIV (human
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
CC syndrome) in a patient. The methods of the invention may also be used to
CC identify agonists or antagonists of the interaction of CCR5 with its
CC natural ligand, and to determine a binding motif for CCR5. The present
CC sequence represents human CCR5
XX
SQ Sequence 352 AA;
Query Match 99.7%; Score 1836; DB 5; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTGVTVTWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFFALKARTVTGVTVTWVAVFASLPGIIFTRSQEGLHYTCSS 180

Db 121 LLTIDRYLAVVHAVFALKARTVTGVTTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 Qy 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKCRNEKKGHRVRLIFTI 240
 Db 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKCRNEKKGHRVRLIFTI 240
 Qy 241 MIVYFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 Db 241 MIVYFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 Qy 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 11
 ABB08343
 ID ABB08343 standard; protein; 352 AA.
 XX
 AC ABB08343;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human chemokine (C-C motif) receptor 5 polypeptide.
 XX
 KW Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 55 /label= Leu, Gln
 FT Misc-difference 182 /label= Phe, Leu
 FT Misc-difference 223 /label= Arg, Gln
 FT
 XX WO200177125-A2.
 PN
 XX 18-OCT-2001.
 XX
 XX 04-APR-2001; 2001WO-US010708.
 XX
 XX 05-APR-2000; 2000US-0194361P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Choi JY, Kliehm SE, Koshy B;
 PI
 XX WPI; 2002-041282/05.
 DR
 DR N-PSDB; ABA97318, ABA97319.
 XX
 XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 FT to diagnose and treat diseases associated with its abnormal expression or
 FT function, including human immunodeficiency virus-1 infection.
 PT
 XX
 XX Claim 29; Fig 3; 61pp; English.
 PS
 XX

XX The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. the CCR5

CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC individual; identifying an association between a trait and a haplotype or
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide
 XX
 XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 5; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLPLFLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGIIFII 120
 Db 61 LKSMTDIYLLNLAIISDLPLFLTPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFGIIFII 120
 QY 121 LUTIDRYLAVVHAVFALKARTVTGVTTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 Db 121 LUTIDRYLAVVHAVFALKARTVTGVTTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 QY 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKCRNEKKGHRVRLIFTI 240
 Db 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKCRNEKKGHRVRLIFTI 240
 QY 241 MIVYFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 Db 241 MIVYFLFWAPYINVLNLTQEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 QY 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 12
 ABR58602
 ID ABR58602 standard; protein; 352 AA.
 XX
 AC ABR58602;
 XX
 DT 09-JUL-2003 (first entry)
 XX
 DE Human cancer related protein SEQ ID NO:259.
 XX
 KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025139-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-US029560.
 XX
 XX 17-SEP-2001; 2001US-0323469P.
 XX 20-SEP-2001; 2001US-0323887P.
 XX 13-NOV-2001; 2001US-0350666P.
 XX 08-FEB-2002; 2002US-0355145P.
 XX 08-FEB-2002; 2002US-0355257P.
 XX 12-APR-2002; 2002US-0372246P.
 XX
 XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72740.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 745; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
XX SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 6; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFIFGFSGIFPII 120
QY 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
DB 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
QY 241 MIVYFLFWAPYNI VLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNI VLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 13
AAO29514
ID AAO29514 standard; protein; 352 AA.
XX
AC AAO29514;
XX
XX 27-AUG-2003 (first entry)
XX

DE Human C-C chemokine receptor type 5 (333) protein.
XX Human; urological disorder; stress urinary incontinence; prostate cancer;
KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
XX
OS Homo sapiens.
XX
XX WO2003039475-A2.
PN
XX 15-MAY-2003.
PD
XX 07-NOV-2002; 2002WO-US035824.
PF
XX 07-NOV-2001; 2001US-0344552P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Silos-Santiago I;
PI
XX WPI; 2003-449396/42.
DR N-PSDB; AAU59912.
XX
XX Identifying a compound, capable of treating urological disorder e.g.,
PT benign prostatic hyperplasia, by assaying the ability of the compound to
PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
PT polypeptide activity.
XX
XX Disclosure; Page 81; 87pp; English.
XX
XX The invention relates to a method for treating a urological disorder
CC which comprises assaying the ability of the compound to modulate 313,
CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
CC activity. The method is useful for identifying a compound for treating an
CC urological disorder comprising urinary incontinence e.g., overactive/
CC oversensitive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central/
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC prostate cancer or kidney disorders. It is also used in gene therapy. The
CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
CC protein. This sequence is used to illustrate the method of the invention
XX
XX SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 6; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFIFGFSGIFPII 120
QY 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
DB 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
QY 241 MIVYFLFWAPYNI VLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNI VLLNTFOEFGNLCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352


```
RESULT 14
ABP97728
ID ABP97728 standard; protein; 352 AA.
XX
XX AC ABP97728;
XX
XX 28-MAY-2003 (first entry)
XX
XX Amino acid sequence of human chemokine receptor CCR5.
XX
XX Human; chemokine receptor; CCR5; viral infection; surface protein;
XX respiratory virus infection; respiratory syncytial virus infection;
XX RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
XX Homo sapiens.
XX
XX WO2003014153-A2.
XX
XX 20-FEB-2003.
XX
XX 12-AUG-2002; 2002WO-CA001248.
XX
XX 10-AUG-2001; 2001US-0311088P.
XX
XX (TOPI-) TOPIGEN PHARM INC.
XX
XX Renzi P, Zenzoumi K;
XX
XX WPI; 2003-256541/25.
XX N-PSDB; ABZ68881.
XX
XX Modulating viral infection of a cell, for treating or preventing
XX respiratory virus infections, bronchitis, pneumonia or asthma, by
XX modulating a binding interaction between a cell chemokine-receptor and a
XX surface protein of the virus.
XX
XX Disclosure; Page 96-98; 120pp; English.
XX
XX The present sequence represents human chemokine receptor CCR5. The
XX specification describes a method for modulating viral infection of a
XX cell. The method comprises modulating a binding interaction between a
XX cell chemokine-receptor and a surface protein of the virus. The proviso
XX is that the cell chemokine-receptor is not CX3CR1 and that the virus is
XX not HIV. The method is useful for treating or preventing respiratory
XX virus infection in vertebrates, more particularly respiratory syncytial
XX virus (RSV) infections, and related diseases, e.g. bronchiolitis,
XX bronchitis, pneumonia or asthma
XX
XX Sequence 352 AA;
XX
Query Match 99.7%; Score 1836; DB 6; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAI S D L F L L T V P F W A H Y L A A Q W D F G N T M C Q L L T G L Y F I G F P S G I F F T I I 120
DB 61 LKSMTDIYLLNLAI S D L F L L T V P F W A H Y A A A Q W D F G N T M C Q L L T G L Y F I G F P S G I F F T I I 120
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DB 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HFYSQVQFQWKNFQTLKIVILGLVPLLVNMVICVSGILKTLLECRNEKRRHRAVLIPTI 240
DB 181 HFYSQVQFQWKNFQTLKIVILGLVPLLVNMVICVSGILKTLLECRNEKRRHRAVLIPTI 240
QY 241 MIVYFLFWAPYNTVLLNTTFQEFGLNCCSSNRLDQAMQVTTGLTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNTVLLNTTFQEFGLNCCSSNRLDQAMQVTTGLTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNTVLLNTTFQEFGLNCCSSNRLDQAMQVTTGLTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGQEISVGL 352
XX
XX RESULT 15
XX ABP81933
XX ID ABP81933 standard; protein; 352 AA.
XX
XX AC ABP81933;
XX
XX 04-MAR-2003 (first entry)
XX
XX Human C-C chemokine receptor 5 protein SEQ ID NO:352.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor; modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.
XX
XX Homo sapiens.
XX
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX N-PSDB; ABZ42781.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
```

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ

Sequence 352 AA;

Query Match	99.7%;	Score 1836;	DB 6;	Length 352;
Best Local Similarity	99.7%;	Pred. No. 3.1e-194;		
Matches 351;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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Db	61	LKSMTDIYLLNLATSDLPFLLTVPFMAHYLAQAQWDFGNTWCQLTGLYFIFGFSGIFFII	120
Qy	121	LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS	180
Db	121	LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS	180
Qy	181	HPYYSQYQFQWKNFOTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKRHRAVRLIFTI	240
Db	181	HPYYSQYQFQWKNFOTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKRHRAVRLIFTI	240
Qy	241	MIYVPLEWAPYNIIVLLNTFQEFGLNCCSSNNELDAQMVTETLGMTHCCINPIIYAFV	300
Db	241	MIYVPLEWAPYNIIVLLNTFQEFGLNCCSSNNELDAQMVTETLGMTHCCINPIIYAFV	300
Qy	301	GEKFRNLLVFFQKHAKRCCKCSIFQQEAPERASSVYTRSTGQEISVGL	352
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Job time : 96 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 07:30:50 ; Search time 90 Seconds
(without alignments)
1623.565 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
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Scoring table: BLOSUM62
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Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1841	100.0	352	16	US-10-700-313-2
3	1841	100.0	352	17	US-10-846-185-2
4	1836	99.7	352	9	US-09-759-841-2
5	1836	99.7	352	9	US-09-813-653-15
6	1836	99.7	352	9	US-09-796-202-1
7	1836	99.7	352	9	US-09-938-719-5
8	1836	99.7	352	9	US-09-939-226-5
9	1836	99.7	352	9	US-09-938-703-5
10	1836	99.7	352	10	US-09-734-221A-14
11	1836	99.7	352	13	US-10-106-623-2
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 15, Appl
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 14, Appl
					Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-439-845-2
; Sequence 2, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347

12	1836	99.7	352	14	US-10-086-814-1	Sequence 1, Appli
13	1836	99.7	352	14	US-10-290-058A-6	Sequence 6, Appli
14	1836	99.7	352	14	US-10-225-567A-352	Sequence 352, App
15	1836	99.7	352	14	US-10-323-314-1	Sequence 1, Appli
16	1836	99.7	352	14	US-10-072-301-1	Sequence 1, Appli
17	1836	99.7	352	14	US-10-071-866-1	Sequence 1, Appli
18	1836	99.7	352	14	US-10-239-423-67	Sequence 67, Appl
19	1836	99.7	352	14	US-10-439-845-4	Sequence 4, Appli
20	1836	99.7	352	15	US-10-360-828-1	Sequence 1, Appli
21	1836	99.7	352	16	US-10-661-798-5	Sequence 5, Appli
22	1836	99.7	352	16	US-10-612-791-5	Sequence 5, Appli
23	1836	99.7	352	16	US-10-772-037-2	Sequence 2, Appli
24	1836	99.7	352	16	US-10-723-860-4095	Sequence 4095, Ap
25	1836	99.7	352	16	US-10-700-313-4	Sequence 4, Appli
26	1836	99.7	352	17	US-10-486-471-10	Sequence 10, Appl
27	1836	99.7	352	17	US-10-846-185-4	Sequence 4, Appli
28	1836	99.7	352	18	US-10-988-485-1	Sequence 1, Appli
29	1836	99.7	352	18	US-10-756-143-5721	Sequence 5721, Ap
30	1836	99.7	352	18	US-10-287-436A-432	Sequence 432, App
31	1836	99.7	352	18	US-10-287-436A-1133	Sequence 1133, Ap
32	1830	99.4	352	9	US-09-813-653-17	Sequence 17, Appl
33	1830	99.4	352	10	US-09-826-509-477	Sequence 477, App
34	1830	99.4	352	14	US-10-164-643-52	Sequence 52, Appl
35	1830	99.4	352	17	US-10-925-095-477	Sequence 477, App
36	1828	99.3	352	9	US-09-725-285-2	Sequence 2, Appli
37	1828	99.3	352	9	US-09-779-879A-22	Sequence 22, Appl
38	1828	99.3	352	9	US-09-779-880A-22	Sequence 22, Appl
39	1828	99.3	352	9	US-09-195-662A-2	Sequence 2, Appli
40	1828	99.3	352	9	US-09-339-912A-2	Sequence 2, Appli
41	1828	99.3	352	9	US-09-502-783A-2	Sequence 2, Appli
42	1828	99.3	352	14	US-10-232-686-2	Sequence 2, Appli
43	1828	99.3	352	14	US-10-067-800-22	Sequence 22, Appl
44	1828	99.3	352	14	US-10-135-839-22	Sequence 22, Appl
45	1828	99.3	352	16	US-10-791-905-2	Sequence 2, Appli

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; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-439-845-2

Query Match 100.0%; Score 1841; DB 14; Length 352;
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Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYIFGFSGIFFII 120
DB 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYIFGFSGIFFII 120
QY 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
DB 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
QY 181 HFPYSQVQFQWKFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HFPYSQVQFQWKFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352

RESULT 2
US-10-700-313-2
; Sequence 2, Application US/10700313
; Publication No. US20040259785A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10700,313
; FILING DATE: 31-Oct-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-10-700-313-2

Query Match 100.0%; Score 1841; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYIFGFSGIFFII 120
DB 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYIFGFSGIFFII 120
QY 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
DB 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
QY 181 HFPYSQVQFQWKFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HFPYSQVQFQWKFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEOEISVGL 352

RESULT 3
US-10-846-185-2
; Sequence 2, Application US/10846185
; Publication No. US20050118677A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/846,185
; FILING DATE: 14-May-2004
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
```

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-846-185-2

Query Match 100.0%; Score 1841; DB 17; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
QY 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYNIIVLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYNIIVLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNVLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNVLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQEIISVGL 352

RESULT 4

US-09-759-841-2
Sequence 2, Application US/09759841
Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Perros, Mancoussos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
QY 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYNIIVLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYNIIVLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNVLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNVLVFFQKHAKRCKCSIFQEQAPERASSVYTRSTGEQEIISVGL 352

RESULT 5

US-09-813-653-15
Sequence 15, Application US/09813653
Patent No. US20020064770A1
GENERAL INFORMATION:
APPLICANT: Nestor, John
APPLICANT: Wilson, Carol
APPLICANT: See, Raymond
APPLICANT: Tan Hehr, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
TYPE: PRT
LENGTH: 352
ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQAQWDFGNTWCQLLTGLYFTGFFSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
DB 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSKQEGHLYTCSS 180
QY 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYQYQFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYNIIVLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352

RESULT 6

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQSSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
Db 1 MDYQSSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTVPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFSGIFFI 120
Db 61 LKSMTDIYLLNLAISDLFLLTVPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFSGIFFI 120
QY 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPYISOYQWKNFQTLKIVILGLVPLVWVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPYISOYQWKNFQTLKIVILGLVPLVWVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352

RESULT 7

US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQSSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
Db 1 MDYQSSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTVPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFSGIFFI 120
Db 61 LKSMTDIYLLNLAISDLFLLTVPFWAHYLAQWDFGNTMCCOLLTGLYFIFGFSGIFFI 120
QY 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPYISOYQWKNFQTLKIVILGLVPLVWVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPYISOYQWKNFQTLKIVILGLVPLVWVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGQEISVGL 352

RESULT 8

US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
QY 61 LKSWTDYLLNLAISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFGFSGIFFII 120
DB 61 LKSWTDYLLNLAISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIFTRSOKEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIFTRSOKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKEHRAVRLIFTI 240
DB 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 9
US-09-938-703-5
Sequence 5, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA

COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
QY 61 LKSWTDYLLNLAISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFGFSGIFFII 120
DB 61 LKSWTDYLLNLAISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIFTRSOKEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIFTRSOKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKEHRAVRLIFTI 240
DB 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 10
US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELLMETTER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

;
;
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,221A
; FILING DATE: 11-Dec-2000
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match 99.7%; Score 1836; DB 10; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
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DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFGPSGIFFTI 120
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DB 121 LITIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPYISOYQPKNFQTLKIVILGLVLLVWVICYSIGILKTLRLCRNEKKRHRVRLIFTI 240
DB 181 HPYISOYQPKNFQTLKIVILGLVLLVWVICYSIGILKTLRLCRNEKKRHRVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVTTGLWTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVTTGLWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 11

US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:

;
;
; APPLICANT: Gray, Patrick W.
; Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20020150888Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 99.7%; Score 1836; DB 13; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFGPSGIFFTI 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFGPSGIFFTI 120
QY 121 LITIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
DB 121 LITIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPYISOYQPKNFQTLKIVILGLVLLVWVICYSIGILKTLRLCRNEKKRHRVRLIFTI 240
DB 181 HPYISOYQPKNFQTLKIVILGLVLLVWVICYSIGILKTLRLCRNEKKRHRVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVTTGLWTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVTTGLWTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 12

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US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match      99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAIASDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIPII 120
DB 61 LKSMTDIYLLNLAIASDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIPII 120
QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
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DB 241 MIYVFLFWAPYNIYLLNTFQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352

RESULT 13
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MP101-289PIRM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match      99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
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DB 61 LKSMTDIYLLNLAIASDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIPII 120
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DB 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYNIYLLNTFQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYNIYLLNTFQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352

RESULT 14
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
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DB 61 LKSMTDIYLLNLAIASDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIPII 120
QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKNFQTLKIVILGLVPLLVNVIYSGILKTLRLCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYNIYLLNTFQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYNIYLLNTFQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEAPEERASSVYTRSTGEQEISVGL 352
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Db 301 GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL 352

RESULT 15
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JFW/MAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDYQVSSPIYDINNYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60

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Db 61 LKSMTDIYLLNLALISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFGFSGIFFII 120

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Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

QY 181 HPFYSQYQFWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLKRCNEKKGHRAVRLIFTI 240
Db 181 HPFYSQYQFWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLKRCNEKKGHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIYLLNTFQEFGLNCCSSNRLDQAMQVETLGNTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFQEFGLNCCSSNRLDQAMQVETLGNTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL 352

Search completed: October 3, 2005, 07:47:26
Job time : 91 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: . October 3, 2005, 07:34:24 ; Search time 28 Seconds
(without alignments)
938.445 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
Sequence: 1 MDYQSSPIYDINYITSEPC.....ERASSVYTRSTGQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1836	99.7	352	3	US-09-087-232A-13
2	1836	99.7	352	3	Sequence 13, Appl
3	1836	99.7	352	3	Sequence 14, Appl
4	1836	99.7	352	3	Sequence 2, Appl
5	1836	99.7	352	4	US-08-833-752-5
6	1836	99.7	352	4	Sequence 5, Appl
7	1836	99.7	352	4	US-09-796-202-1
8	1836	99.7	352	4	Sequence 1, Appl
9	1836	99.7	352	4	US-09-938-719-5
10	1836	99.7	352	4	Sequence 5, Appl
11	1830	99.4	352	4	US-08-771-276-2
12	1828	99.3	352	4	US-09-502-783A-2
13	1828	99.3	352	4	Sequence 2, Appl
14	1828	99.3	352	4	US-09-339-912A-2
15	1828	99.3	352	4	Sequence 2, Appl
16	1821	98.9	352	3	US-09-195-662A-2
17	1809	98.3	352	3	US-08-466-343D-2
18	1802	97.9	352	4	Sequence 5, Appl
19	1541	83.7	354	3	US-08-771-276-20
20	1360	73.9	360	4	US-08-724-984A-2
21	1359	73.8	347	1	US-09-131-827A-20
22	1359	73.8	360	1	US-08-461-244-3
23	1359	73.8	360	3	US-08-450-393A-4
24	1359	73.8	360	3	US-08-446-669-4
25	1359	73.8	360	3	US-09-045-583-50
26	1359	73.8	360	4	US-09-534-185-50
27	1359	73.8	360	4	US-09-131-827A-2
					Sequence 4, Appl

28 1359 73.8 360 5 PCT-US95-00476-4 Sequence 4, Appl
29 1359 73.8 377 4 US-09-949-016-11221 Sequence 11221, A
30 1353 73.5 360 4 US-09-826-509-473 Sequence 473, App
31 1345 73.1 360 4 US-08-833-752-7 Sequence 7, Appl
32 1345 73.1 360 4 US-09-938-719-7 Sequence 7, Appl
33 1345 73.1 360 4 US-09-939-226B-7 Sequence 51, Appl
34 1340 72.8 360 3 US-09-045-583-51 Sequence 51, Appl
35 1340 72.8 360 4 US-09-534-185-51 Sequence 9, Appl
36 1219 66.2 344 3 US-08-466-343D-9 Sequence 9, Appl
37 1219 66.2 344 4 US-09-502-784A-9 Sequence 9, Appl
38 1219 66.2 374 1 US-08-450-393A-2 Sequence 2, Appl
39 1219 66.2 374 3 US-08-446-669-2 Sequence 2, Appl
40 1219 66.2 374 4 US-10-039-659A-14 Sequence 14, Appl
41 1219 66.2 374 4 US-09-625-573-2 Sequence 2, Appl
42 1219 66.2 374 5 PCT-US95-00476-2 Sequence 2, Appl
43 1219 66.2 387 4 US-09-949-016-11222 Sequence 11222, A
44 1133.5 61.6 329 4 US-09-502-783A-9 Sequence 9, Appl
45 1133.5 61.6 329 4 US-09-339-912A-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-087-232A-13

Query Match 99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 1;
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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-861-105-14

Query Match          99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILINCKR 60

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QY 121 LTTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LTTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180

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Db 181 HPYSQYQFWKQNFQTLKIVILGLVPLLVWVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFOEFGNLCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
```

```
RESULT 2
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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```
RESULT 3
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6285184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1662
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHAKRFCKCCSIPOQEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHAKRFCKCCSIPOQEAPERASSVYTRSTGEQEISVGL 352

RESULT 4

US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 648375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-5

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHAKRFCKCCSIPOQEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHAKRFCKCCSIPOQEAPERASSVYTRSTGEQEISVGL 352

RESULT 5

US-09-796-202-1
Sequence 1, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: OLSON, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPVFWAHYLAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPYSQYQFWKQFQTLKIVILGLVPLLVVVICYSGLKTLRCRNEKKEHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHAKRFCKCCSIPOQEAPERASSVYTRSTGEQEISVGL 352

Db 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 6
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. 6692938
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFSGIFFII 120
QY 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCKRKRHRVRLIFTI 240
Db 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCKRKRHRVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQFQFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIYVFLFWAPYINVLNLTQFQFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

Db 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 7
US-08-771-276-2
; Sequence 2, Application US/08771276
; Patent No. 6797811
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 679781land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
US-08-771-276-2

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFSGIFFII 120
QY 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCKRKRHRVRLIFTI 240
Db 181 HPFYSQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCKRKRHRVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQFQFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIYVFLFWAPYINVLNLTQFQFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

Db 301 GEFERNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQBIISVGL 352

RESULT 8

US-09-939-226B-5
; Sequence 5, Application US/09939226B
; Patent No. 6800447
; GENERAL INFORMATION:
; APPLICANT: Euroscreen S.A.
; APPLICANT: SAMSON Michel
; APPLICANT: PARMENTIER, Marc
; APPLICANT: VASSART, Gilbert
; APPLICANT: LIBERT, Fredrick
; TITLE OF INVENTION: Methods for Identifying Compounds which Bind the Active CCR5 Chem
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 9409/2023C
; CURRENT APPLICATION NUMBER: US/09/939,226B
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 08/833,752
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 09/626,939
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 08/810,028
; PRIOR FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-226B-5

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVIFGFGVGNMVLILINCKR 60
Db 1 MDQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVIFGFGVGNMVLILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFFLLTPFWFAHYLAAQWDFGNTWCQLLTGLYFGFGSIFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPFWFAHYLAAQWDFGNTWCQLLTGLYFGFGSIFII 120
QY 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
Db 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
QY 181 HFPYSQYQWKNFQTLKIVILGLVPLLVNVICYSGLKTLTLRCNEKKHRAVRLIFTI 240
Db 181 HFPYSQYQWKNFQTLKIVILGLVPLLVNVICYSGLKTLTLRCNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIIVLLNTFOEPFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFOEPFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQBIISVGL 352
Db 301 GEFERNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQBIISVGL 352

RESULT 9

US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/045,583
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 99.4%; Score 1830; DB 3; Length 352;
Best Local Similarity 99.1%; Pred. No. 3.6e-146;
Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVIFGFGVGNMVLILINCKR 60
Db 1 MDQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLSVIFGFGVGNMVLILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFFLLTPFWFAHYLAAQWDFGNTWCQLLTGLYFGFGSIFII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPFWFAHYLAAQWDFGNTWCQLLTGLYFGFGSIFII 120
QY 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
Db 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
QY 181 HFPYSQYQWKNFQTLKIVILGLVPLLVNVICYSGLKTLTLRCNEKKHRAVRLIFTI 240
Db 181 HFPYSQYQWKNFQTLKIVILGLVPLLVNVICYSGLKTLTLRCNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIIVLLNTFOEPFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFOEPFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQBIISVGL 352
Db 301 GEFERNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQBIISVGL 352

RESULT 10

US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP

QY 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 13

US-09-502-784A-2

; Sequence 2, Application US/09502784A

; Patent No. 6743594

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Methods of Screening Using Human G-Protein

; FILE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)

; FILE REFERENCE: 1488.1150005

; CURRENT APPLICATION NUMBER: US/09/502.784A

; CURRENT FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Version 3.1

; SEQ ID NO 2

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

; OTHER INFORMATION: Deduced Amino Acid Sequence

US-09-502-784A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 14

US-09-339-912A-2

; Sequence 2, Application US/09339912A

; Patent No. 6759519

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

; FILE OF INVENTION: (CCR5 Receptor)

; FILE REFERENCE: 1488.1150003

; CURRENT APPLICATION NUMBER: US/09/339,912A

; CURRENT FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: 09/195,662

; PRIOR FILING DATE: 1998-11-18

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Artificial Sequence: Genomic

; FEATURE:

; OTHER INFORMATION: Deduced Amino Acid Sequence

US-09-339-912A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFPII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
Db 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTQEFPLGNNCSSNRLDQAMQVETLGTTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 15
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match      99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVIFRGFVGNMLVILILINCKR 60

QY      61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
Db      61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120

QY      121 LLTIDRYLAVVHAVFALKARTVTFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db      121 LLTIDRYLAVVHAVFALKARTVTFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180

QY      181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRAVRLIFTI 240
Db      181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRAVRLIFTI 240

QY      241 MIVYFLFWAPYNIIVLLNTFQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db      241 MIVYFLFWAPYNIIVLLNTFQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY      301 GEKFRNYLLVFFOKHIAKRECKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db      301 GEKFRNYLLVFFOKHIAKRECKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
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